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GenCore version 5.1.3
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OM protein - protein search, using sw model

November 30, 2002, 12:33:53; Search time 12.5 Seconds Run on:

(without alignments) 3868.449 Million cell updates/sec

1 MSGKSFKAGVCPPKKSAQCL.....IEQNTKSPLFMGKVVNPTQK 503 US-10-025-514-8 2675 Perfect score: Sednence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database:

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | 0 | | 1 - | alpha-1-antitrupei | 4 . | ٠. | ٠. | - 1 | | | alpha-1-antitronsi | | alpha-1 prototoses | alpha-1-antiprotes | alpha-1 proteinage | alpha-1-antiprotoi | alpha 1-proteinsco | - | | alpha-1-antitronsi | alpha-1-antiprotoi | Contranein precure | | alpha 1-proteines | | serine proteinese | alpha-1-antichumot | Contransta procure | kallikrein-binding | corticosteroid-bin |
|-----------|---------------|--------|--------|--------------------|--------|--------|---------|--------|--------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------|-------------------|--------|-------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ΩI | ITHO | ITBA | ITRI | ITSH | 860036 | \$21097 | JX0346 | 149470 | 149471 | I49452 | S54981 | 149472 | JX0154 | 149473 | JX0267 | 156481 | 149474 | A54968 | ITMSC | A39088 | C39088 | B39088 | A45457 | A28882 | I50494 | ITHUC | JX0129 | B29131 | 2832 |
| | 80 | ٦ | | | | | | 7 | | | | | | | | | | | | | | | | | | | | | | |
| | Length | 418 | 409 | 411 | 416 | 413 | 416 | 406 | 413 | 402 | 413 | 413 | 413 | 413 | 413 | 413 | 413 | 413 | 413 | 412 | 405 | 410 | 388 | 410 | 420 | 410 | 433 | 418 | 416 | 405 |
| dР | Ouery | 76.7 | 71.4 | 54.9 | | 54.5 | 54.1 | 51.8 | | | 50.3 | | 50.1 | | | | | | 48.9 | | | | | | | | | | 30.9 | |
| | Score | 2052.5 | 1909.5 | 1467.5 | 1465.5 | 1458.5 | 1447.5 | 1386 | 1347 | 1346 | 1345 | 1343.5 | 1341 | 1339.5 | 1328 | 1326.5 | 1323 | 1319.5 | 1308.5 | 1306 | 1293 | 1246 | 1187.5 | 1165 | 1157.5 | 845 | 830 | 829 | 826.5 | 820 |
| | Result No. | ٦ | 6 | m | 4 | S | 9 | 7 | æ · | 0 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 |

| corticosteroid-bin | protein C inhibito | correction Front Courses along a long along the course and course and contract and | serine proteinase | kallikrein-binding thyroxine-bindina | serine proteinase | thyroxine-binding | serine proteinase | serine proteinase alpha-1-antitrypsi |
|--------------------|--------------------|---|-------------------|---|-------------------|-------------------|-------------------|---|
| 153281 S23675 | A39339 A49518 | A36117 JH0494 | \$11320 | S19/24 I46421 | S08102 A49190 | A47224 A39567 | S31507 | 531505 150492 |
| 0.0 | 0 0 | 0 0 | ~ | 7 7 | 0 0 | 00 | (| 9 (9 |
| 406 418 | 406 | 383 | 408 | 417 | 403 | 415 | 418 | 372 |
| 30.6 | 30.5 | 30.3 | 30.3 | 30.1 | 30.0 29.8 | 29.4 | 28.8 | 27.6 |
| 819.5 818 | 816 816 | 811 810.5 | 810 | 804 | 803 796 | 787.5 | 771.5 | 739 |
| 30 | 33 33 | 34 35 | 36 | 38 | 39 4 0 | 417 | 43 | 4.0 |

ALIGNMENTS

| | 88.011.9 J |
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| | . in a neutrypsin precursor (validated) - human |
| | N;Alternate names: alpha-1-AT; alpha-1-proteinase inhibitor |
| | C;Species: Homo sapiens (man) |
| | C;Date: 30-Nov-1980 #sequence_revision 31-Mar-1992 #text change 15-Sep-2000 |
| | C; Accession: A21853; B21853; A93352; A90944; A58528; A23174; A93281; A32336; S14476. |
| | R; Long, G.L.; Chandra, T.; Woo, S.L.C.; Davie, E.W.; Kurachi, K |
| | Biochemistry 23, 4828-4837, 1984 |
| | A, Title: Complete sequence of the cDNA for human alpha-1-antitrynsin and the concept |
| | A; Reference number: A21853; MUID: 85047190; PMID: 6093867 |
| | A; Accession: A21853 |
| | A; Molecule type: mRNA |
| | A; Residues: 1-418 <lon1></lon1> |
| | A; Cross-references: GB: K02212; NID: a177830 |
| | A; Experimental source: M (normal) allele |
| | A; Accession: B21853 |
| | A; Molecule type: DNA |
| | A; Residues: 1-287,'V', 289-418 <lon2></lon2> |
| _ | A; Cross references: GB: K02212; NID: q177830; PIDN: AAB59495.1: PID: q177831 |
| | A; Experimental source: S variant allele |
| | R; Rosenberg, S.; Barr, P.J.; Najarian, R.C.; Hallewell, R.A. |
| | Nature 312, 77-80, 1984 |
| | A; Title: Synthesis in yeast of a functional oxidation-resistant mutant of human alpha |
| | A; Reference number: A93352; MUID:85036645; PMID:6387509 |
| | A; Accession: A93352 |
| | A; Molecule type: mRNA |
| _ | The state of the s |

A; Residues: 1-124, 'H', 126-325,'I', 327-418 <ROS>A; Cross-references: EMBL: X01683; NID: 928965

R;Bollen, A.; Herzog, A.; Cravador, A.; Herion, P.; Chuchana, P.; Vander Straten, A.; A;Tellen, A.; Herzog, A.; Cravador, A.; Herion, P.; Chuchana, P.; Vander Straten, A.;Telle: Cloning and expression in Escherichia coli of full-length complementary DNA A;Reference number: A90944; MUID:84107980; PMID:6319097

A; Molecule type: mRNA
A; Residues: 1-138, DG', 141-272, NV', 274-418 <BOL>
A; Residues: 1-138, DG', 141-272, NV', 274-418 <BOL>
A; Cross-references: GB: K01396; NID: 928965
A; Note: this sequence has been corrected in reference A58528
A; Note: this sequence has been corrected in reference A58528
B; Colau, B.; Chuchana, P.; Bollen, A.
A; Title: Revised sequence of full-length complementary DNA coding for human alpha-1-a
A; Reference number: A58528; MUID: 8502667; PMID: 6333329
A; Contents: corrections to sequence in A90944
A; Recession: A58528
A; Molecule type: mRNA
A; Residues: 1-418 <COL>

A.Cross-references: GB.K01396; NID:g28965; PIDN:CAA25838.1; PID:g28966
R.Ciliberto, G.; Dente, L.; Cortese, R.
Cell 41, 531-540, 1985
A.Fitle: Cell-specific expression of a transfected human alpha-1-antitrypsin gene.
A.Reference number: A23174; MUID:85176977; PMID:2985281

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76.7%; Score 2052.5;
    A; Accession: I39372
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A; Residues: 44-53;384-392 <DEN>
R; Residues: 44-53;384-392 <DEN>
R; Dengler, R.; Lottspeich, F.; Derthuer, W.; Mast, A.E.; Emmerich, B.
Biol. Chem. Hoppe-Seyler 376, 165-172, 1995
A; Title: Limited proteolysis of alpha(1)-proteinase inhibitor (alpha(1)-PI) in acute leu
A; Reference number: S55249; MUID:95336645; PMID:7612193
A; Accession: S55249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 292-418 <RIL>
A; Cross-references: EMBL:X02920; NID:g24437; PIDN:CAA26677.1; PID:g24438
B; Schulze, A.J.; Baumann, U.; Knof, S.; Jaeger, E.; Huber, R.; Laurell, C.B.
Eur. J. Blochem. 194, 51-56, 1990
A; Title: Structural transition of alpha(1)-antitrypsin by a peptide sequentially similar
A; Reference number: $13833; MUID:91071209; PMID:2253623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Isolation and serine protease inhibitory activity of the 44-residue, C-terminal A;Reference number: S23516; MUID:93024095; PMID:1406456 A;Accession: S23516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Sequence homology and structural comparison between the chromosomal human alpha
A;Reference number: 139371; MUID:82220035; PMID:6979715
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: peptide sequence differences with A21853 (Leu-200 and the amidation states of re R;Zhu, X.J.; Kang, S.S.; Hargrove, K.; Shochat, D.; Jarrells, M.; Mojesky, M.; Chan, S.R B;Zhu, X.J.; Kang, S.S.; Hargrove, K.; Shochat, D.; Jarrells, M.; Mojesky, M.; Chan, S.R Biochem. J. 246, 25-36, 1987
A;Title: The identification of epitopic sites in human alpha-1-proteinase inhibitor.
A;Reference number: A32336; MUID:88049621; PMID:2445337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Weiland, K.L.; Falany, C.N.; Dooley, T.P.
Submitted to the EMBL Data Library, December 1989
A;Description: Identification of a cDNA encoding a variant form of the human proteolytiq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Cass-references: EMBL:X17122; NID:g28636; PIDN:CAA34982.1; PID:g28637
A; Experimental source: a variant form
A; Experimental source: a variant form
A; Experimental source: a variant form
A; Filey. J.H.; Bathurst, I.C.; Edbrooke, M.R.; Carrell, R.W.; Craig, R.K.
FEBS Lett. 189, 361-366, 1985
A; Title: Alpha-1-antitrypsin and serum albumin mRNA accumulation in normal, acute phase
A; Reference number: A24013; MUID:86005469; PMID:3876243
                                                                                                      var
A; Reference 1-11,13-173,'H',175-228,'D',230-418 <CIL>
A; Coss-treferences: GB: M11465; NID:g177826; PIDN:AAA51546.1; PID:g177827
A; Note: the authors state that this sequence corresponds to the M (normal) allele; 3 var. R; Carrell, R.W; Deppson, J.O.; Laurell, C.B.; Brennan, S.O.; Owen, M.C.; Vaughan, L.; Nature 298, 329-334, 1982
A; Title: Structure and variation of human alpha-1-antitrypsin.
A; Reference number: A93281; MUID: B2220135; PMID: 7045697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein, F.; Plewan, A.; Ogilvie, A.; Emmerich, B. B; Dengler, R.; Eger, G.; Lottspeich, F.; Plewan, A.; Ogilvie, A.; Emmerich, B. Biol. Chem. Hoppe-Seyler 373, 581-588, 1992 A; Title: Proteolytic inactivation of alpha (1) proteinase inhibitor in vivo: detection, A; Molecule number: $23962; MulD: 92384968; PMID: 1515087 A; Accession: $23962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 25-28;43-47;207-208;382-389;414-418 <DE2>
R;Leicht, M.; Long, G.L.; Chandra, T.; Kurachi, K.; Kidd, V.J.; Mace, M.
Nature 297, 655-659, 1982
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A; Molecule type: protein
A; Residues: 25-41 < CSCH>
A; Residuen: A. Narkates, A.J.; Miller, E.J.
Matrix 12, 233-241, 1992
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A;Molecule type: DNA
A;Residues: 1-67 <LEI1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A32336
A; Molecule type: protein
A; Residues: 25-418 <ZHU>
                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 25-418 <CAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: I39371
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A. Accession: 19370
A. Accession: 19370
A. Accession: 19370
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: mRW
A. Molecule type: m
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F:24-ALP/roduct: alpha-1-antitrypsin #status experimental <AMAT>
F:70:107.271/Binding site: carbohydrate (Asn) (covalent) #status experimental F:382/Inhibitory site: Met (elastase, collagenase) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 371-385 <CHA>
R; Coutelle, C.; Speer, A.; Rogers, J.; Kalsheker, N.; Humphries, S.; Williamson, F Coutelle, C.; Speer, 44, 421-431, 1985
B; Diomed. Blochlim. Acta 44, 421-431, 1985
A; Title: Construction and partial characterization of a human liver cDNA library. A; Reference number: 139370; MUID: 85225507; PMID: 3873938
A; Accession: 139370
                                                                                                                                            A, Molecule type: DNA
A, Robicule type: DNA
A, Residues: 196-225 < LEI2>
A, Residues: 196-225 < LEI2>
A, Cross-references: GB:J00066; NID:g177819; PIDN:AAB59370.1; PID:g177823
B, Cromay, W.S.W.; Wardell, M.R.; Lomas, D.A.; Carrell, R.W.
Biochem. J. 314, 647-653, 1996
A, Title: Probing serpin reactive-loop conformations by proteolytic cleavage.
A, Reference number: S63599; MUID:96239126; PMID:8670081
A; Cross-references: GB:J00064; NID:g177817; PIDN:AAB59369.1; PID:g177822
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A;Introns: 216/1; 306/2; 355/3
A;Note: the first intron occurs before the initiator codon
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: GDB:PI
A,Cross-references: GDB:120289; OMIM:107400
                                                                                                                 A; Status: translated from GB/EMBL/DDBJ
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Length 418;

DB 1;

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A;Wolecule type: mRNA
A;Residues: 188-246, T',248-321, D',323-389 <FLI>
A;Cross_references: BmBL:X16273; NID:957299; PION:CAA34349.1; PID:9930263
A;Crusumi, Y.; Sohda, M.; Ohkubo, K.; Takami, N.; Oda, K.; Ikehara, Y.
J. Blochem. 108, 230-234, 1990
A;Title: Molecular cloning and sequencing of the cDNA of rat alpha-1-protease inhibit
A;Reference number: JX0123; MUID:91035351; PMID:2229024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary tar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N'Alternate names: alpha-I-proteinase inhibitor
C'Species: Rattus norvegicus (Norway rat)
C'Date: 31-Mar-1992 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000
C'Accession: A38992; B3892; S08016; JV30123; A38823
R'Chao, S.; Chai, K.X.; Chao, L.; Chao, J.
Biochemistry 29, 323-329, 1990
A;Title: Molecular cloning and primary structure of rat alpha-1-antitrypsin.
A;Reference number: A33892; MUID:90148955; PMID:2302382
                                                                                                                      336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                         396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                      C. Superfamily: antithrombin III
C.Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F.1-24/Domain: signal sequence #status predicted <SIG>
F.25-411/Product: alpha-1-antitrypsin #status experimental <MAT>
F.64,101,265/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;376/Inhibitory site: Met (elastase, collagenase) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 QLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQEL 208
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A;Accession: B33892
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A; Residues: 1-13, 'G',15-83, 'V', 85-247, 'Y', 249-317, 'N', 319-411 <MIS>
A; Cross-references: GB:D00675; NID:9220648; PIDN:BAA00579.1; PID:9220649
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                                                                                                                                                                                                                                                                                                                                                               456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                         Library, August 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 25-57 CCH2>
R; Filnk, I.L.; Balley, T.; Morkin, E.
submitted to the EMBL Data Library, A.
A; Reference number: S08016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-1-antitrypsin precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: serum A; Accession: A38823
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A; Residues: 25-45 <M12>
C; Comment: Alpha-1-antitr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 4-411 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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Nighter a unitary print precurate.
Nighter a unitary print precurate.
C:Species: Papio sp. (baboon)
C:Species: Papio sp. 
                                                                                         96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                         156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                                                                                                         216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                   276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               psin.
C.Superfamily: antithrombin III
C.Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
C.Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F;16-409/Product: alpha-1-antitrypsin #status predicted <AMAT>
F;51,98,262/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 GWCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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      97.8%; Pred. No. 3.1e-127;
tive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-1-antitrypsin precursor - baboon (fragment)
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Matches 368; Conservative
                         Matches 399; Conservative
Best Local Similarity
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C;Accession: S60036
R;Nakatanl, T.; Suzuki, Y.; Yoshida, K.; Sinohara, H.
Biochim. Biophys. Acta 1263, 245-248, 1995
A;Title: Molecular cloning and sequence analysis of cDNA encoding plasma alpha-1-anti A;Reference number: S60036; MUID:96004896; PMID:7548212
A;Reference number: S60036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-1-antitrypsin precursor - bovine
N.Alternate names: alpha-1-proteinase inhibitor; proteinase inhibitor Inh3
N.Alternate names: alpha-1-proteinase inhibitor; proteinase inhibitor Inh3
C;Species: Bos primigenius taurus (cattle)
C;Accession: S21097; PC2040; S18920
R;Sinha, D.; Bakhshi, M.R.; Kirby, E.P.
Biochim, Biophys. Acta 1130, 209-212, 1992
A;Title: Complete cDNA sequence of bovine alpha1-antitrypsin.
A;Reference number: S21097; WUID:92223096; PMID:1562597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: BMBL:D49709; NID:g1088432; PIDN:BAA08557.1; PID:g1794155 A;Cross-references: BMBL:D49709; NID:g1088432; PIDN:BAA08557.1; PID:g1794155 A;Note: the source is designated as Syrian hamster C;Superfamily: antithrombin III
E;1-24/Domain: signal sequence #status predicted <SIG>F;25-413/Product: alpha-1-antitrypsin #status predicted <MAT>
                                                                                                                                                                                                                                                 N;Alternate names: alpha-1-antiproteinase
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 DSQLQLTTGNGLFLSECLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
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302 YASSANLHIPKLSISETYDLKTVLGELGINRVFSNGADLSGITEEQPLMVSKALHKAALT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                            54.5%; Score 1458.5; DB 2; Length 413; 68.6%; Pred. No. 3e-88;
                                                     449 IDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56; Mismatches
                                                                                                                                                                                                                                         alpha-1-antitrypsin precursor - golden hamster
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A; Residues: 1-413 <NAK>
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A;Note: the authors translated the codon ATC for residue 395 as Ala
C;Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.; Wu, Y. Nucleic Acids Res. 17, 6398, 1989
A;Title: Nucleotide and deduced amino acid sequence of sheep alpha-1 antitrypsin. A;Reference number: S05312; MUID:89366677; PMID:2788872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-1-antitrypsin precursor - sheep N;Alternate names: alpha-1-proteinase inhibitor C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) C;Species: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 DRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLT 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVP 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 QLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQEL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 RDLKCCMGMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 KIAHQSNTSNIFFSPVSIASAFAMLSLGAKGNTHTEILEGLGFNLTELAEAEIHKGFQHL 121
                                             209 LRTLNOPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQIND 268
                                                                       269 YVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVP 328
                                                                                                                                                                         329 MMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENE 388
                                                                                                                                                                                                                                                                                                 238 MMNRLGMFDMHYCSTLSSWVLAMDYLGNATAIFLLPDDGKMQHLEQTLTKDLISRFLLNR 297
                                                                                                                                                                                                                                                                                                                                                   389 DRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLT 448
                                                                                                                                                                                                                                                                                                                                                                                298 QTRSAILYFPKLSISGTYNLKTLLSSLGITRVFNNDADLSGITEDAPLKLSQAVHKAVLT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 IDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQ 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 416;
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54.8%; Score 1465.5; Di
Best Local Similarity 67.6%; Pred. No. 1e-88;
Matches 280; Conservative 62; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S05312
A; Molecule type: mRNA
A; Residues: 1-416 <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S05312
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Matches 271; Conservative
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                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: alpha-1 PI-1
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A: Molecule type: mRNA
A: Residues: 1-416 <SINA
A: Residues: 1-416 <SINA
A: Residues: 1-416 <SINA
A: Cross-references: EMBL: X63129; NID: 941; PIDN: CAA44840.1; PID: 942
A: Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 209-Thi S: Sinha, D.; Yang, X.; Emig, F.; Kirby, E.P.
J. Biochem. 115, 387-391, 1994
A: Title: Isolation and characterization of two protease inhibitors from bovine plasma. A: Reference number: PX0072; MUID: 94334275; PMID: 8056747
A: Accession: PC2040
A: Molecule type: protein
A: Residues: 25-44 <SIZ>
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JADDA-1-antiproteinase precursor - Mongolian jird
C;Species: Meriones unquiculatus (Mongolian jird)
C;Species: Apr-1995 #sequence_revision 26-May-1995 #text_change 28-May-1999
C;Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 28-May-1999
C;Date: 22-Apr-1995 #sequence_revision 26-May-1999
C;Date: Jackhari, Y.: Yoshida, K.: Yamamoto, K.: Sinohara, H.
J: Blochem. 116, 582-588, 1994
A;Title: Plasma alpha-1-antiproteinase from the Mongolian gerbil, Meriones unguiculatus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                             C; Superfamily: antithrombin III
C; Keywords: acute phase; 91ycoprotein; plasma; serine proteinase inhibitor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-416/Product: alpha-1-antitrypsin #status predicted <MAT>
F;68,105,143,269/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 RDLKCCMGMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 QLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQEL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 LRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQIND 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 YVEKGTOGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVP 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 MMKRLGMENIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 DRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 RGLILLAALC---CLAPISLAGVLQGHAVQETDDTSHQE--AACHKIAPNLANFAFSIYH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:S77822; NID:g998663; PIDN:AAB33367.1; PID:g998664
A;Accession: PC2357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449 IDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQ 502
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F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-406/Product: alpha-1-antiproteinase #status predicted <MAT>
F;383-387/Region: serpin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                       70; Indels
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A;Residues: 25-44;77-96 <002>
A;Experimental source: plasma
C;Superfamily: antithrombin III
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A; Residues: 1-406 <GOT>
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NAlternate names: all pha-1-antitrypsin
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 149470; A25495
R;Borriello, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A;Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary A;Reference number: 149470; MUID:92052104; PMID:1946354
F;59,96,134,260,403/Binding site: carbohydrate (Asn) (covalent) #status predicted F;371/Inhibitory site: Met (trypsin, chymotrypsin, elastase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Krauter, K.S.; Citron. B.A.; Hsu, M.T.; Powell, D.; Darnell Jr., J.E.
DNA 5, 29-36, 1986
A;Title: Isolation and characterization of the alpha-1-antitrypsin gene of mice.
A;Reference number: A25495; MUID:86163765; PMID:3007061
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                                                                                                                                                                                               96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                                                                                                                            156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                                                                                                                                                                                                            216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                                                                                                        Indels 14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
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A;Molecule type: mRNA
A;Residues: 1-413 <RES>
A;Cross-references: GB:M75721; NID:9191841; PIDN:AAC28869.1; PID:9191842
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A;Residues: 211-245,'D',247-322,'L',324-403,'V',405-413 <KRA>
A;Cross-references: GB:M12586; NID:9192092; PIDN:AAA51624.1; PID:9192094
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                                                                                              DB 2; Length 406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQ 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.8%; Score 1386; DB 2;
66.6%; Pred. No. 1.7e-83;
tive 58; Mismatches 64;
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alpha-1-antiproteinase isoform E precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-oct-1996 #sequence_revision 07-Feb-1997 #text_change 20-Jun-2000
C;Accession: 534981; #72199
R;Saito, A.: Sinobara, H.
Biochem. J. 307, 369-375, 1995
A.Title: Rabbit alpha-1-antiproteinase E: a novel recombinant serpin which does not i
A;Reference number: 554981; MUID:95251597; PMID:7733871
A;Accession: 554981
A;Welecule type: mRMA.
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                                                                                                                                                                                                                A;Title: Complete cDNA sequence and chromosomal localization of mouse alpha-1-antitry A;Reference number: 149452; MUID:90152670; PMID:2303252 A;Accession: 149452 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                   C; Accession: I49452
R;Sifers, R.N.; Ledley, F.D.; Reed-Fourquet, L.; Ledbetter, D.H.; Ledbetter, S.A.; Genomics 6, 100-104, 1990
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A;Cross-references: EMBL:D17725; NID:g1008927; PIDN:BAA04579.1; PID:g1008928
A;Accession: S72199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 FNIQHCKKLSSWVLLMKYLGNATAIFFLFDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 LDVHHCSTLSSWYLLMDYAGNASAVFLLPEDGRWQHLEGTLNKELISKILLURRRRLVQI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus_musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 DSQLQLITGNGLFLSEGLKLYDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEBEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 GLC---CLVPSFLAED-----VQETDTSQKDQS-PASHEIAINLGDFAISLYRELVHQSN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M25529; NID:g191549; PIDN:AAA37132.1; PID:g309079 C;Superfamily: antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                           50.3%; Score 1345; DB 2; Length 413; 62.6%; Pred. No. 8.4e-81; trive 71; Mismatches 72; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455 EAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
354 EAAAAIVFEAVPMSMPPILRFDHPFLFIIFEEHTQSPIFVGKVVDPTHK 402
                                                                                                            alpha-1-antitrypsin precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 25-33;374-387 <SAI2>
C; Superfamily: antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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A; Residues: 1-413 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-1 proteinase inhibitor 2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.3%; Score 1346; DB 2; Length 402;
62.6%; Pred. No. 7e-81;
tive 71; Mismatches 72; Indels 10; Gaps
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                                                                                                                                                                                                                                                 336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                      245 LHVHHCSTLSSWVLLMDYAGNATAVFLLPDDGKMQHLEQTLSKELISKFLLNRRRLAQI 304
                                                                                                                                                                                                                                                                                                                               396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGT 454
                                                                                                                                                                                                                                                                                                                                                       216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDXVEKGTQ 275
                                                                                                                                                                GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                          65 TSNIFFSPVSIATAFAMLSLGSKGDTHTQILEGLQFNLTQTSEADIHKSFQHLLQTLNRP 124
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                 455 EAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                455 EAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
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A; Residues: 1-402 <RES>
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R;Saito, A.; Sinohara, H.
J. Biochem. 109, 158-162, 1991
A;Title: Cloning and sequencing of CDNA coding for rabbit alpha-1-antiproteinase F: a
A;Reference number: JX0154; MUID:91201273; PMID:2016265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-1 proteinase inhibitor 4 - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: Mus musculus (sequence_revision 02-Jul-1996 #sequence_revision 02-Jul-1996 #sequence_revision 02-Jul-1996 #separence_revision 02-Jul-1996 #separence_revision 02-Jul-1996 #separence_revision 02-Jul-1996 #text_change 16-Jul-1999 R; Borriello, F; Krauter, K.S. Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991 A; Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary
                                                                                                                                                                                                                                                                                                                                                      C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 21-Jul-2000
                                     336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                          396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGT 454
                                                                                                                                        97 MCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNS 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 LAGLGCLLP-----GFLADEAQETAVSSHEQDHPACHRIAPSLAEFALSLYREVAHESNT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-413 <SAI>
A;Cross-references: GB:X57710; NID:g1455; PIDN:CAA40881.1; PID:g1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.1%; Score 1339.5; DB 2; Length 413; 62.8%; Pred. No. 1.9e-80; Live 64; Mismatches 82; Indels 5;
                                                                                                                                                                                            455 EAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                    ||| ::| |||:|| 367 AGATYMEIIPMSLPDSITLDRPFLFVIYSHEIKSPLFVGKVVDPTQ 412
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                                                                                                                                                                                                                                                                                                                                       alpha-1-antiproteinase F - rabbit
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R: Borriello, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A/Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary dive
A; Reference number: 149470; MuID: 92052104; PMID: 1946354
A; Accession: 149472
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
                                                                                                                   97 MCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNS 156
                                                                                                                                                                                               157 TNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPD 216
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F;25-413/Product: alpha-1-antiproteinase E #status experimental <MAT>
                                                  DB 2; Length 413;
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                                                                                      83; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.2%; Score 1343.5; DB 63.3%; Pred. No. 1.1e-80 tive 61; Mismatches 8:
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                                                        Best Local Similarity 63.38 Matches 257; Conservative
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C;Superfamily: antithrombin III
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A; Residues: 1-413 <RES>
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C; Superfamily: antithrombin III
C; Superfamily: antithrombin III
C; Superfamily: approprice in the sequence #status predicted <SIG>
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-413/Product: alpha-1-antiproteinase S-1 #status experimental <WAT>
F; 55-102, 266/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 LDVHHCSMLSSWVLLMDYAGNTTAVFLLPDDGKMQHLEQTLNKELISQFLLNRRKSDAQI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                       96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GLC---CLVPSFLAED-----VQETDISQKDQS-PASHEIATNLGDFALRLYRELVHQSN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JX0267
A; Molecule type: mRNA
A; Residues: 1-413 <SAI>
A; Cross references: GB:D16104; NID:g286191; PIDN:BAA03678.1; PID:g303762
A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                       Indels 10; Gaps
                                                                                                                                A; Cross-references: GB:M75718; NID:g191847; PIDN:AAC28867.1; PID:g191848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

49.6%; Score 1326.5; DB 2; Length 413;
Best Local Similarity 63.1%; Pred. No. 1.4e-79;
Matches 256; Conservative 60; Mismatches 85; Indels 5;
                                                                                                                                                                                                                                                                   49.6%; Score 1328; DB 2; Length 413; 61.9%; Pred. No. 1.1e-79; tive 70; Mismatches 76; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
A; Reference number: 149470; MUID:92052104; PMID:1946354
                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                             A;Gene: alpha-1 PI-4
C;Superfamily: antithrombin III
                                                                                                                                                                                                                                                                                                                             Matches 253; Conservative
                                                                                                                                                                                                                                                                                                       Best_Local Similarity
                                                                                         A; Molecule type: mRNA
A; Residues: 1-413 <RES>
                                    A; Accession: I49473
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365
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217 SQLQLITGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDXVEKGTQG 276
                                                                                                                              277 KIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMF 336
                                                                                                                                                                                            337 NIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLH 396
                                                                                                                                                                                                               247 VKFHCSTLASTVLRMDYKGNATALFLLPDEGKLQHLEDTLTTELTAKFLAKSSFRSVRVR 306
                                                                                                                                                                                                                                                                             397 LPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEA
                                                                                                                                                 457 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQ 502
                                                                                                                                                                                                                                                                                                                                              Search completed: November 30, 2002, 12:37:28
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